PP-091 Non-specific immune therapy and hepatitis B and chronic asymptomatic carriers to obtain HBV-DNA negative effect relationship

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Objective: Observation of chronic hepatitis B and asymptomatic carriers to obtain HBV-DNA negative efficacy and non-specific immune response relationship.
Methods: 255 cases of patients will be divided into 4 group; observation lamivudine and Mycobacterium FU36 with Chinese medicine group (A) and lamivudine with the Chinese group (B), HBV-DNA on the efficacy, safety and efficacy issues, 3 month course of treatment, follow-up 9 months.
Results: 1) B group of chronic hepatitis B have HBV-DNA, respectively, 30.30% and 26.47% of the significant efficiency, it was significantly higher than non-carriers of asymptomatic has a case to obtain the effect markedly, P<0,01; 2) A group of chronic hepatitis B in HBV-DNA were 82.75% and 76.66% of the significant efficiency, was significantly higher than group B, only 30.30% and 26.47% efficiency of the significant, P <0,01; 3) A group of HBeAg negative carriers of asymptomatic HBV-DNA has the remarkable efficiency of 80.64%, significantly higher than the B group is not an case,A group of HBeAg-positive carriers of asymptomatic HBV-DNA, only 5.71% of the significant efficiency, P<0,01, etc. Course of treatment there is no adverse reaction.
Conclusions: Non-specific immune status changes, and abnormal alanine aminotransferase, and HBV-DNA was markedly effect the results significantly correlated, induced HBeAg-specific immune tolerance of HBV-DNA to obtain the effect of markedly present only for the "impact" role.

PP-092 Novel role of peripheral blood mononuclear cells in HBV intrauterine infection

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Background & aims: Intrauterine infection by HBV represents an integral cause for the failure of hepatitis B vaccines. This study aimed at appreciating the role played by PBMC in HBV intrauterine infection.
Methods: Serum samples were taken from study subjects to detect HBsAg, HBV DNA in serum and in PBMC. For mother-to-fetus PBMC transfer,AS-PCR and heminested-PCR assays for insertion/deletion polymorphisms involving glutathione *S*-transferase M1 (GSM1) and angiotensin-converting enzyme (ACE) were employed.
Results: A total of 119 mother-baby pairs were identified as clinically informative cases from 312 mothers and their newborn infants. 75 showed HBV-infected PBMC traffic from mother to fetus. Among these 75 infants, 61 were HBV-infected intrauterinely, and 57 carried HBV-infected PBMC. Statistical analysis demonstrated that maternal PBMC HBV infection was associated with HBV intrauterine infection (OR=4.20, 95% CI:2.01-8.85; $P<0.01$). Our date suggested that PBMC transfer from mother to fetus was positively connected with the risk of HBV intrauterine infection (OR=8.42, 95% CI: 3.32-21.61; $p<0.0001$). Such fetomaternal PBMC transfer was also positively allied with the risk of HBV infection of PBMC in infants (OR=9.51, 95%CI: 3.71-24.91; $p<0.0001$). However, no significant association was found between mother-to-fetus PBMC transmission and the newborns' serum HBV DNA or HBsAg positivity.
Conclusions: Our results are supportive of the conclusion that maternal PBMCs infected with HBV contribute to HBV intrauterine infection of newborn infants by transferring from mother to fetus.

PP-093 Analysis of genes ralted to cholesterol metabolism differentially expressed in HepG2 cells transfected with HBV-replicon

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Background: To explore the changes in gene expressions in the HepG2 cell transfected by HBV replicon.
Method: A 22000 gene DNA microarray was used to examine gene expressions in the HepG2 cell transfected by HBV replicon. The differentially expressed genes were identified and some genes which maybe contribute to Cholesterol metabolism were subjected to realtime PCR analysis.
Result: The differentially expressed genes mostly involved in transcription regulatory molecules, cytokines, signal transduction, protein,glucose, lipid metabolism. The results of Real-time PCR of 7DCR, NADH-b5R were consistent with that of genechip analysis.
Conclusion: Microarray expression profile of HepG2 cell transfected by HBV replicon is differential. 7DCR, NADH-b5R may play an important role in cholesterol metabolism.

PP-094 Screening of the target genes transactivated by PS1TP2 protein with suppression subtractive hybridization technique

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Background: To construct a subtractive cDNA library of genes transactivated by PS1TP2 protein with suppression subtractive hybridization (SSH) technique and clone genes associated with transactivation.
Methods: Suppression subtractive hybridization technique and bioinformatics technique were used, the mRNA was isolated from HepG2 cells transfected with pcDNA3.1(−)-PS1TP2 and pcDNA3.1(−) empty vector respectively; cDNA was synthesized. After digestion with restriction enzyme RsaI, cDNA fragments were obtained. Tester cDNA was then divided into two groups and ligated to the specific adaptor 1 and adaptor 2 respectively. After tester cDNA was hybridized with driver cDNA twice and underwent two times of nested PCR, amplified cDNA fragments were subcloned into pGEM-Teasy vectors to set up the subtractive library. Amplification of the library was carried out with *E. coli* strain DH5α. The cDNA was sequenced and analyzed in GenBank with Blast search after PCR.
Results: The subtractive library of genes transactivated by PS1TP2 was constructed successfully.The amplified library contains 90 positive clones.Colony PCR showed that 60 clones contain 200∼1000 bp inserts. Sequence analysis was performed in 25 clones randomly, and the full length sequences were obtained with bioinformatics method and searched for homologous DNA sequence from GenBank, altogether 15 coding sequences were gotten.
Conclusion: The obtained sequences may be target genes transactivated by PS1TP2 protein among which some genes coding proteins involved in cell cycle regulation, metabolism, immunity and cell apoptosis. This finding brought some clues for studying the biological functions of PS1TP2.

PP-095 Sequence analysis of Hepatitis B Virus S gene 'a' epitope in HBV infected patients positive for both HBsAg and HBsAb

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Objective: To characterize the sequence of hepatitis B virus S gene 'a' epitope in HBV infected patients positive for HBsAg and HBsAb.